

gi | 146231940 | ref | NP_001078927.1 | MDDSE-VESTASILASVKEQEAQFEKLRTRALEEERRHVSAQLERVRVSPDANPLMANGTLRRHONGRFGVDADLERQKFSDLKLNQPDHSHLLYSTIPRMOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 114642290 | ref | XP_001140660.1 | MDDSE-VESTASILASVKEQEAQFEKLRTRALEEERRHVSAQLERVRVSPDANPLMANGTLRRHONGRFGVDADLERQKFSDLKLNQPDHSHLLYSTIPRMOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 73982248 | ref | XP_849632.1 | MDDSE-VESTASILASVKEQEAQFEKLRTRALEEERRHVSAQLERVRVSPDANPLMANGTLRRHONGRFGVDADLERQKFPDLKLNQPDHSHLLYSTIPRMOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 194673532 | ref | XP_593164.4 | MDDSE-VESPASILLASVKEQEAQFEKLRTRALEEERRHVSAQLERVRVSPDASPLLANGTLRRHONGRFGVDADLERQKFSDLKLNQPDHSHLLYSTIPRMOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 83745122 | ref | NP_031641.2 | MDDSE-VESTASILASVKEQEAQFEKLRTRALEEERRHVSAQLERVRVSPDANSLMANGTLRRHONGRFGVDADLERQKFSDLKLNQPDHSHLLYSTIPRMOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 109468364 | ref | XP_242062.4 | -----MOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 118091411 | ref | XP_001232051.1 | MAATQPALRRAPLVNPPVMIISLSSLAIGSQILPSSPAQVRRRRRIRGEAR---DPNPPGCSQNGRFLGDADLERQKFPDLKLNQPDHSHLLYSTIPRMOEPGQIVET--YTEDPEGAMSVVSVETSDDGTTRRTTETVKKVVKI 150
gi | 292609897 | ref | XP_684691.4 | ---MEQCENAAASLLASVREQEMQFERLTRALEEERRSVGPGSGLTPRPLP-----TLONGRIQDAELERLKLSEGYING-----IQVRMLDPGHIVES-VTVESDPHEALPIIIVETGDDGTTRRTTETVKKVVKI 150
gi | 292609900 | ref | XP_002660581.1 | ---MEQCENAAASLLASVREQEMQFERLTRALEEERRSVGPGSGLTPRPLP-----TLONGRIQDAELERLKLSEGYING-----IQVRMLDPGHIVES-VTVESDPHEALPIIIVETGDDGTTRRTTETVKKVVKI 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi | 146231940 | ref | NP_001078927.1 | VTTRIVQPVAMPDGLPVDAS-SVS--NNYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MEGYRAPSRG--DVGYPQPVVRVGGSSVDL---HRFHPPEPYGLE 300
gi | 114642290 | ref | XP_001140660.1 | VTTRIVQPVAMPDGLPVDAS-SVS--NNYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MEGYRAPSRG--DVGYPQPVVRVGGSSVDL---HRFHPPEPYGLE 300
gi | 73982248 | ref | XP_849632.1 | VTTRIVQPVAMPDGLPVDAS-SVS--NNYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MEGYRAPSRG--DVGYPQPVVRVGGSSVDL---HRFHPPEPYGLE 300
gi | 194673532 | ref | XP_593164.4 | VTTRIVQPVAMPDGLPVDAS-AVS--NSYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MEGYRAPSRG--DVGYPQPVVRVGGSSVDL---HRFHPPEPYGLE 300
gi | 83745122 | ref | NP_031641.2 | MTTRIVQPVAMPDGLPVDAS-AVS--NNYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MEGYRAPSRG--DVGYPQPVVRVGGSSVDL---HRFHPPEPYGLE 300
gi | 109468364 | ref | XP_242062.4 | MTTRIVQPVAMPDGLPVDAS-AVS--NNYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MEGYRAPSRG--DVGYPQPVVRVGGSSVDL---HRFHPPEPYGLE 300
gi | 118091411 | ref | XP_001232051.1 | VTTRIVQPVAMPDGLPVDAS-PVT--SNYIQLGRDFRKNNGGGPGYVGOAGTATLPRNFHYPPDGYSRHYEDGYPGGSNDYGLSRVTRIEERYRPS-----MDAYRAPSRG--DIYGPQPVVRVGGSSVDL---NHFFPEPYGLE 300
gi | 292609897 | ref | XP_684691.4 | VTTRIVQPVSVS--DTLSLDGIGSVTGMFVSNSPMDRVRVPP--PGPMDYP---TSVPRNYHYGPPAGYDDYRSVPP---SEAYTSLRGTMRDDRYRFPVGYRILDSAVRTRHSRPLDYPYSAQPVGRMGSAVEIHALQRFVPEPYGLE 300
gi | 292609900 | ref | XP_002660581.1 | VTTRIVQPVSVS--DTLSLDGIGSVTGMFVSNSPMDRVRVPP--PGPMDYP---TSVPRNYHYGPPAGYDDYRSVPP---SEAYTSLRGTMRDDRYRFPVGYRILDSAVRTRHSRPLDYPYSAQPVGRMGSAVEIHALQRFVPEPYGLE 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi | 146231940 | ref | NP_001078927.1 | DDORSMGYDLDYGM--MSDYGTRARRTGTP--SDPRRRLRSYEDMIGEEVP--SDQYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 114642290 | ref | XP_001140660.1 | DDORSMGYDLDYGM--MSDYGTRARRTGTP--SDPRRRLRSYEDMIGEEVP--SDQYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 73982248 | ref | XP_849632.1 | DDORSMGYDLDYGM--MSDYGTRARRTGTP--SDPRRRLRSYEDMIGEEVP--SDQYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 194673532 | ref | XP_593164.4 | DDORSMGYDLDYGM--MSDYGTRARRTGTP--SDPRRRLRSYEDMIGEEVP--SDQYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 83745122 | ref | NP_031641.2 | DDORSMGYDLDYGM--MSDYGTRARRTGTP--SDPRRRLRSYEDMIGEEVP--PDQYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 109468364 | ref | XP_242062.4 | DDORSMGYDLDYGM--MSDYGTRARRTGTP--SDPRRRLRSYEDMIGEEVP--PDQYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 118091411 | ref | XP_001232051.1 | DDORSVGFDDVDYGL--MSDYGTRARRAGTP--SDARRRLRSYEDMIVDEVA--PDRYYW--APLAQHERGSLASLDSLRRKGGPPPPNWRQPELPEVIAMLGFRLLDAVKSNAAYLQHLCYRNDKVKIDVRKLGKIPVLVGLLDHPKKEV 450
gi | 292609897 | ref | XP_684691.4 | DDORSLGYDEPDYGMGPAMHYSMPRLAHPHAPPVRRRTGSEYETLDGMSGAGDMFYWGGGAPLAQGERGSMASLDSLTRKGPAPTAWRQPELPEVIAMLNRLDPVKSNAAYLQHLTFKNDKVKSEVRRLKGPALVSMLDNPKKEV 450
gi | 292609900 | ref | XP_002660581.1 | DDORSLGYDEPDYGMGPAMHYSMPRLAHPHAPPVRRRTGSEYETLDGMSGAGDMFYWGGGAPLAQGERGSMASLDSLTRKGPAPTAWRQPELPEVIAMLNRLDPVKSNAAYLQHLTFKNDKVKSEVRRLKGPALVSMLDNPKKEV 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450



gi | 146231940 | ref | NP_001078927.1 | HLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDCKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 114642290 | ref | XP_001140660.1 | HLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDCKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 73982248 | ref | XP_849632.1 | HLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDCKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 194673532 | ref | XP_593164.4 | HLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDCKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 83745122 | ref | NP_031641.2 | HLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDCKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 109468364 | ref | XP_242062.4 | HLGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDCKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 118091411 | ref | XP_001232051.1 | HYGACGALKNISFGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTEVITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDSKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 292609897 | ref | XP_684691.4 | HYGACGALKNISYGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTDITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDSKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
gi | 292609900 | ref | XP_002660581.1 | HYGACGALKNISYGRDQDNKIAIKNCDGVPALVRLLRKARDMDLTDITGLTNLNSHSDSIKMEIVDHALHALDDEVIIIPHSGWEREPP--EDSKPRHIEWESVLTNTAGCLRNVSSESEARRKLRCCDGLVDALIFIVQAEIGQKDS 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi | 146231940 | ref | NP_001078927.1 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 114642290 | ref | XP_001140660.1 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 73982248 | ref | XP_849632.1 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 194673532 | ref | XP_593164.4 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 83745122 | ref | NP_031641.2 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 109468364 | ref | XP_242062.4 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 118091411 | ref | XP_001232051.1 | DSKLVENCVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 292609897 | ref | XP_684691.4 | DNKLIENSVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
gi | 292609900 | ref | XP_002660581.1 | DNKLIENSVCLLRNLSYQVHREIPQAERYOEAPPVANNTPGHAASCFGAKKGDWFSRGGKPIEDPANDTVDFPKRTSPARGYELLPOPEVVRVIYISLLKESKTPAILEASAGAIQNLCAGRWYGRYIRRSALROEKALSATADLLN 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi |146231940|ref|NP_001078927.1|EHERVVKAASGALRNLAVDARNKELIGKHAI PNLVKNLPGGQON-SSWNFS EDTVISILNTINEVIAENLEAAKKLRETGGIEKLVLINKSGNRS EKEVRAAALVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRSQSSHSDSTL 900
gi |114642290|ref|XP_001140660.1|EHERVVKAASGALRNLAVDARNKELIGKHAI PNLVKNLPGGQON-SSWNFS EDTVISILNTINEVIAENLEAAKKLRETGGIEKLVLINKSGNRS EKEVRAAALVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRSQSSHSDSTL 900
gi |73982248|ref|XP_849632.1|EHERVVKAASGALRNLAVDARNKELIGKHAI PNLVKNLPGGQON-SSWNFS EDTVISILNTINEVIAENLEAAKKLRETGGIEKLVLINKSGNRS EKEVRAAALVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRSQSSHSDSTL 900
gi |194673532|ref|XP_593164.4|EHERVVKAASGALRNLAVDARNKELIGKHAI PNLVKNLPGGQON-SSWNFS EDTVISILNTINEVIAENLEAAKKLRETGGIEKLVLINKSGNRS EKEVRAAALVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRSQSSHSDSTL 900
gi |83745122|ref|NP_031641.2|EHERVVKAASGALRNLAVDARNKELIGKHAI PNLVKNLPGGQON-SSWNFS EDTVISILNTINEVIAENLEAAKKLRETGGIEKLVLINKSGNRS EKEVRAAALVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRSQSSHSDSTL 900
gi |109468364|ref|XP_242062.4|EHERVVKAASGALRNLAVDARNKELIGKHAI PNLVKNLPGGQON-SSWNFS EDTVISILNTINEVIAENLEAAKKLRETGGIEKLVLINKSGNRS EKEVRAAALVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRSQSSHSDSTL 900
gi |118091411|ref|XP_001232051.1|DSERVVKAASGALRNLAVDLRNKELIGKHAI PNLVKNLPGGQON-PAKNSLSEDTVVSILNTINEVIVDNLEAAKKLRETGGIEKLVLINKSGNRS EREVRAAAVLOTIWGYKELRKP LEKEGWKKSDFQVNLNNA SRTQGN SFDSTL 900
gi |292609897|ref|XP_684691.4|GNDRVVRAAMS GALRNLAIDARNRELIGKHAVPNLVANLPGGGQSQPARALSEETVVSIVLS TMAEVVGS SVDAAKTLRSA GIERLRLVINKDSNRSDREV RGAGLVLIIVWGFKELRRTLEKDGWKKTFDMVNLNPPNNTRENGGYEESTL 900
gi |292609900|ref|XP_002660581.1|GNDRVVRAAMS GALRNLAIDARNRELIGKHAVPNLVANLPGGGQSQPARALSEETVVSIVLS TMAEVVGS SVDAAKTLRSA GIERLRLVINKDSNRSDREV RGAGLVLIIVWGFKELRRTLEKDGWKKTFDMVNLNPPNNTRENGGYEESTL 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi |146231940|ref|NP_001078927.1|PLIDRNQKSDKKPDREEIQMSNMGSNKSLDNNYSTPNERGDHNR TLDRSGDLGDMPELKG TPLMQDEGQESLEBEELDVLVLDDEGGQVSYPSMOKI-- 1000
gi |114642290|ref|XP_001140660.1|PLIDRNQKSDKKPDREEIQMSNMGSNKSLDNNYSTPNERGDHNR TLDRSGDLGDMPELKG TPLMQDEGQESLEBEELDVLVLDDEGGQVSYPSMOKI-- 1000
gi |73982248|ref|XP_849632.1|PLIDRNQKTDKPPDREEIQMSMGSNTKSLDNNYSTLNERGDHNR TLDRSGDLGEMPELKG TPLMQDEGQESLEBEELDVLVLDDEGGQVSNPSMOKI-- 1000
gi |194673532|ref|XP_593164.4|PLIDRSQRSDKKPDREEIQMSMGSNTKSLDNNYSTLNERGDHNR TLDRPGDLGEMPELKG -APLMQDEGQESLEBEELDVLF LD -EGEPMSCPAMOKI-- 1000
gi |83745122|ref|NP_031641.2|PLIDRNQKSDKKPDREEIQMSNMGSNKSLDNNYSTLNERGDHNR TLDRSGDLGDMPELKG ----- -APLMOKI-- 1000
gi |109468364|ref|XP_242062.4|PLIDRNQKSDKKPDREEIQMSNMGSNKSLDNNYSTLNERGDHNR TLDRSGDLGDMPELKG ----- -APLMOKI-- 1000
gi |118091411|ref|XP_001232051.1|PLIDRNQKTD ----- NYSTLNEM -DSR TLDRSGDLGDMPELKG -APLMQDEGQESQPE ----- AEE SDAVFS PASOKI-- 1000
gi |292609897|ref|XP_684691.4|PLIDRGGKQDR -EKDM I PLNDIG -PBAYSTIDRGRRL -TLDD I LDRS DRDAPQG - -GMYGERRGSLPLLDSDYDC 1000
gi |292609900|ref|XP_002660581.1|PLIDRGGKQDR -EKDM I PLNDIG -PBAYSTIDRGRRL -TLDD I LDRS DRDAPQG - -I 1000
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000

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